In the specification:

Please amend the specification as follows:

1. At pages 7-8; bridging paragraph:

The promoter sequence of the present invention is preferably selected from a group consisting of base sequences represented by ~~SEQ. ID. No 2 ~ No 11~~ SEQ ID NOS:2-11. The promoter sequence represented by SEQ. ID. No 11 is a whole promoter sequence located in front of transcription beginning region (ATG) included in peroxidase SWPA4 genomic gene derived from a sweetpotato which is represented by SEQ. ID. No 1. SEQ. ID. No 2, SEQ. ID. No 3, SEQ. ID. No 4, SEQ. ID. No 5, SEQ. ID. No 6, SEQ. ID. No 7, SEQ. ID. No 8, SEQ. ID. No 9 and SEQ. ID. No 10 are all fragment sequences located on the –110th, -177th, -306th, -366th, -433rd, -818th, -1199th, -1467th and –1934th sites each from the end of a whole SWPA4 promoter sequence (located just in front of transcription beginning region).

2. At pages 10-11; bridging paragraph:

In the preferred embodiment of the invention, the present inventors prepared promoter sequences represented by ~~SEQ. ID. No 2 ~ No 11~~ SEQ ID NOS:2-11 from peroxidase SWPA4 genomic gene represented by SEQ. ID. No 1 included in a sweetpotato, and an expression vector containing the same. Transgenic tobacco cells including various size promoters were also produced by transfecting tobacco culture cells with the expression vector prepared above. An activity of the promoter was investigated by using protoplasts of tobacco cells. As a result, deleted promoter fragments having different sizes, which were represented by ~~SEQ. ID. No 2 ~ No 11~~ SEQ ID NOS:2-11, showed similar activity to or over 4.5-fold (but less than 8.5-fold) higher promoter activity than CaMV35S promoter of a control group (see FIG. 3a and 3b). A

transgenic tobacco plant was produced by inserting an expression vector containing various size deleted promoter fragments into a tobacco leaf section using Agrobacterium. Then, stress was induced therein. Promoter activity was investigated after inducing stress. As a result, the activity of GUS (a target gene included in an expression vector) was increased after the treatment of pathogenic bacteria, methyl viologen or causing wound, at least twice as much as before the treatment (see Table 1). Therefore, promoter sequences of the present invention represented by ~~SEQ. ID. No 2 ~ No 11~~ SEQ ID NOS:2-11 were proved to have higher promoter activity than any conventional promoters, and the activity was strongly enhanced by stress. So, promoter sequences of the present invention can be effectively used for the development of an environmental stress-resistant plant and the production of valuable substances by taking an advantage of the transgenic plant cells obtained thereby.

3. At page 12; first full paragraph:

The promoter sequence included in the expression vector of the present invention is preferably selected from base sequences represented by ~~SEQ. ID. No 2 ~ No 11~~ SEQ ID NOS:2-11.

4. At pages 12-13; bridging paragraph:

It is also preferred for a target substance of the invention to include various proteins or peptides having pharmaceutical effects or any other substance giving resistance against stress to a transformant. In the preferred embodiment of the present invention, expression vectors having deletion promoters in various sizes were constructed by cloning each sequence of the promoter represented by ~~SEQ. ID. No 2 ~ No 11~~ SEQ ID NOS:2-11 into plasmid vector pBI1221 (CaMV35S promoter, GUS coding sequence and NOS transcription terminator sequence were included) provided by Clontech, Co. Each expression vector prepared above was named,

according to the length of a promoter sequence, 'p2433', 'p1934', 'p1467', 'p1199', 'p818', 'p433', 'p366', 'p306', 'p177' and 'p110'. GUS was used as a target gene for the expression vector of the invention. But, GUS could be replaced by any other target valuable substance coding sequence to construct an expression vector producing a target valuable substance keeping resistance against stress.

5. At page 13; second full paragraph:

For the preparation of transgenic cells and a transgenic plant of the present invention, the expression vector preferably contained a promoter sequence selected from a group consisting of sequences represented by ~~SEQ. ID. No 2 - No 11~~ SEQ ID NOS:2-11. For producing transgenic cells of the present invention, a host cell was preferably selected from a group consisting of tobacco, major agricultural crops such as rice, sweetpotato, etc, and medicinal plants including ginseng. For producing a transgenic plant of the present invention, a host plant was preferably selected from a group consisting of tobacco, major crops such as rice, sweetpotato, etc, and medicinal plants including ginseng.

6. At pages 13-14; bridging paragraph:

In the preferred embodiment of the present invention, cells of a tobacco, Nicotiana tabacum, were transfected with expression vectors p110, p177, p306, p366, p433, p818, p1199, p1467, p1934 and p2433, each including a promoter sequence selected from a group consisting of sequences represented by ~~SEQ. ID. No 2 - No 11~~ SEQ ID NOS:2-11, using an Agrobacterium, resulting in the preparation of transgenic tobacco cells expressing the above expression vectors respectively. Among those transgenic cells, the one cell line that was transfected with expression vector p1467 showed the highest promoter activity, so that it was named 'p1467

(Nicotiana tabacum cv. Xanthi) cell line' and deposited at KCTC (Korean Collection for Type Culture) of KRIBB (Korea Research Institute of Bioscience and Biotechnology) on February 10, 2004 (Accession No: KCTC 10594BP).

7. At pages 14-15; bridging paragraph:

1) Constructing an expression vector containing each of a promoter sequence selected from a group consisting of base sequences represented by ~~SEQ. ID. No 2 ~ No 11~~ SEQ ID NOS:2-11, a target valuable substance coding sequence and a transcription terminator sequence; and

8. At pages 20-21; bridging paragraph:

As a result, SWPA4 promoter was confirmed to have regulatory elements of various eukaryotic promoters, and TATA-box for the translation starting was located between -92 ~ -86 (Zhu, Q. et al., Plant Cell, 14, 795-803, 2002). RSTGACTMANA (SEQ ID NO:31) (Lucibello, FC. et al., Oncogene, 8, 1667-1672, 1993), a consensus sequence of AP1, which has been known as a relevant factor responding to active oxygens and a transcription regulatory protein is attached to, was located between -431 ~ -421. TTGACC (Rushton, PJ. et al., EMBO J, 15, 5690-5700, 1996), a consensus sequence of ELRE which strongly induces a gene expression by elicitor generated by a defense mechanism against germ infection or wound in plants, was found between -2227 ~ -2232, and between -1329 ~ -1334 as an inverted repeat sequence. TAACGTA (Sutoh, K. et al., Plant J, 34, 636-645, 2003), a consensus sequence of GARE whose expression is regulated by gibberellin (GA), a plant hormone in a plant, was located between -382 ~ -376. AWTTCAAA (Itzhaki, H. et al., Proc Natl Acad Sci USA, 91, 8925-8929, 1994), a consensus sequence of ERE whose expression is regulated by ethylene, a plant hormone related to ripening and aging of a fruit of a plant, was located between -192 ~ -185.

W-box (Yu, D. et al., Plant Cell, 13, 1527-1540, 2001), to which WRKY protein expressed by salicylic acid playing an important role in resistance against diseases is attached, was located as a repeat sequence of TTGAC at two regions between –1993 and –1989 and between –1032 and –1028, and located as an inverted repeat sequence at two other regions between –2227 and –2231 and between –1329 and –1333. AGAAN (Fernandes, M. et al., Nucleic Acids Res, 22, 167-173, 1994), a consensus sequence of HSE (heat shock element) responding to heat shock was located between –182 and –178 of the promoter (FIG. 1a).